Figure 9a

GAP of: Czaal47.Seq check: 446 from: 1 to: 1214
    to: Axig1complete.Con check: 928 from: 1 to: 3123

Symbol comparison table:
Gencoredisk: [Gcgcore.Data.Rundata]Nwsgapdna.Cmp
 CompCheck: 8760

```
        Gap Weight:      50   Average Match: 10.000
     Length Weight:       3   Average Mismatch:  0.000

         Quality:  10871         Length:    3123
           Ratio:  8.955          Gaps:        3
Percent Similarity: 100.000   Percent Identity: 100.000

        Match display thresholds for the alignment(s):
                 |  = IDENTITY
                 :  =   5
                 .  =   1
```

Czaal47.Seq x Axig1complete.Con May 11, 2000 12:05   ..


```
    1 ................................GCAGGAACTTAT 12
                                     ||||||||||||
 1101 CGCGTCACTCACGGGTAGCTCATGGTCGAGCGTAGCATGCAGGAACTTAT 1150

   13 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 62
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1151 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 1200

   63 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTCAGCTAGCTAGCTGCG 112
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1201 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTCAGCTAGCTAGCTGCG 1250

  113 CCGTGACCACGCACATGACCGCAGTGCGCGCGGGGCTGATCAAGGGAAAG 162
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1251 CCGTGACCACGCACATGACCGCAGTGCGCGCGGGGCTGATCAAGGGAAAG 1300

  163 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 212
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1301 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 1350

  213 CGCTGGCTGCCGCCGCCGAGTTCGTCGGTCTCCTCAGCAGCTCGGCTGGC 262
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1351 CGCTGGCTGCCGCCGCCGAGTTCGTCGGTCTCCTCAGCAGCTCGGCTGGC 1400

  263 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 312
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1401 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 1450

  313 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 362
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1451 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 1500
```

Figure 9b

```
 363 ACCGCGACCGCGACGGCGTCGTCGACCATGAACAGCAAAGCAACAA....  408
     ||||||||||||||||||||||||||||||||||||||||||||||
1501 ACCGCGACCGCGACGGCGTCGTCGACCATGAACAGCAAAGCAACAAGTGA 1550



 409 ........................TGTACCCAGGAAGAAGAGGCTGG  431
                             |||||||||||||||||||||||
1601 CCCAAATCCGATCCGTGGTGTGTGTAGTGTACCCAGGAAGAAGAGGCTGG 1650

 432 TGGGGTGGCCGCCGGTGAAGTGCGCGCGTAGGCGTAGCTGCGGCGGCGGG  481
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1651 TGGGGTGGCCGCCGGTGAAGTGCGCGCGTAGGCGTAGCTGCGGCGGCGGG 1700

 482 TACGTGAAGGTGAAGCTGGAAGGGGTGCCCATCGGGCGGAAGGTGGACGT  531
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1701 TACGTGAAGGTGAAGCTGGAAGGGGTGCCCATCGGGCGGAAGGTGGACGT 1750

 532 GTCCATCCACGGCTCGTACCAGGAGCTGCTCCGCACGCTCGAGAGCATGT  581
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1751 GTCCATCCACGGCTCGTACCAGGAGCTGCTCCGCACGCTCGAGAGCATGT 1800

 582 TCCCTTCGGGTAACCAACA.............................  600
     ||||||||||||||||||
1801 TCCCTTCGGGTAACCAACAAGGTGCGTACGTTCCCGGGCCGCGGCGAGCC 1850



 601 ...........................................AG  602
                                                ||
1951 CTCCCGGCACTTAACTTGGTCGCATATACTATTCCTGTAACCTCTGGCAG 2000

 603 ATCATGCAGAAGACGAGGTGGTGGTCTCGCACGAGCGCCGCCGTCGCCAT  652
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2001 ATCATGCAGAAGACGAGGTGGTGGTCTCGCACGAGCGCCGCCGTCGCCAT 2050

 653 CCTTATGTAGTCACCTACGAGGACGGCGAAGGGGACTGGTTGCTCGTCGG  702
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2051 CCTTATGTAGTCACCTACGAGGACGGCGAAGGGGACTGGTTGCTCGTCGG 2100

 703 AGATGATGTGCCGTGGGA...........................  720
     ||||||||||||||||||
2101 AGATGATGTGCCGTGGGAGTACGTATCAGTCACTACTACTGTCGTCTGTA 2150



 721 ............................GGTCTTTGTCAAGTCAGTG  739
                                 ||||||||||||||||||
2201 GAACTTAAAAACGACGTTGATTTCCTTGCAGGGTCTTTGTCAAGTCAGTG 2250

 740 AAGCGGCTCAAGATACTTGCGTAGCCGACGGTCGGCGCCTCAGAGACGTC  789
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2251 AAGCGGCTCAAGATACTTGCGTAGCCGACGGTCGGCGCCTCAGAGACGTC 2300
```

Figure 9c

```
 790 GTGTGGTCCGTCTCACCAGGATCGGAGCAGTGTAGTACTCCTGGGCGTCA 839
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2301 GTGTGGTCCGTCTCACCAGGATCGGAGCAGTGTAGTACTCCTGGGCGTCA 2350

 840 TCTGCGTAATAACGTTGTTTCTGTCCTGTGTGCCCGTAGCAGTACGTACT 889
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2351 TCTGCGTAATAACGTTGTTTCTGTCCTGTGTGCCCGTAGCAGTACGTACT 2400

 890 GTCCTATAGTAAGCTAGCTTTATGGGGTGCTTCAGCTTTCAGAGCATGAC 939
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2401 GTCCTATAGTAAGCTAGCTTTATGGGGTGCTTCAGCTTTCAGAGCATGAC 2450

 940 GAAAGCACTGATTAGCTGCTGTCATCACATTTGGTTCGTCTTTGTGTCGT 989
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2451 GAAAGCACTGATTAGCTGCTGTCATCACATTTGGTTCGTCTTTGTGTCGT 2500

 990 ACGGTATCGCTGGCGTCAGTGTCGCGGCAGCCTAGGTGATCTAAGCATAC 1039
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2501 ACGGTATCGCTGGCGTCAGTGTCGCGGCAGCCTAGGTGATCTAAGCATAC 2550

1040 TTACTATCTCAAGTTACTTTTGGTTTCCTGAGCTTGCATGGTAATTCATA 1089
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2551 TTACTATCTCAAGTTACTTTTGGTTTCCTGAGCTTGCATGGTAATTCATA 2600

1090 TACCGTATACGTGTGTGACTCAGGGGCGAAGCTGCCTTAAGGCACAGGGG 1139
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2601 TACCGTATACGTGTGTGACTCAGGGGCGAAGCTGCCTTAAGGCACAGGGG 2650

1140 TCACCGGACCCGATGGAATTTATCAAATCCAGTGTAAAATACTATTTAAC 1189
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2651 TCACCGGACCCGATGGAATTTATCAAATCCAGTGTAAAATACTATTTAAC 2700

1190 ACTGTTCATCAATATATTTGATTTC......................... 1214
     |||||||||||||||||||||||||
2701 ACTGTTCATCAATATATTTGATTTCAATAATTCATGGAGCTGACCTTGTG 2750
```